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## RAW SEQUENCE LISTING

DATE: 04/08/2002

PATENT APPLICATION: US/10/003,671A

TIME: 15:14:37

Input Set : A:\36858Aseq.txt

Output Set: N:\CRF3\04082002\J003671A.raw

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5 <110> APPLICANT: MIZE, ET AL  
8 <120> TITLE OF INVENTION: NOVEL INTERLEUKIN-1 HY2 MATERIALS AND METHODS  
11 <130> FILE REFERENCE: 28110/36858A  
14 <140> CURRENT APPLICATION NUMBER: US 10/003,671A  
C--> 15 <141> CURRENT FILING DATE: 2002-03-22  
17 <150> PRIOR APPLICATION NUMBER: US 60/245,346  
18 <151> PRIOR FILING DATE: 2000-11-02  
20 <160> NUMBER OF SEQ ID NOS: 26  
23 <170> SOFTWARE: PatentIn version 3.1  
26 <210> SEQ ID NO: 1  
27 <211> LENGTH: 998  
28 <212> TYPE: DNA  
29 <213> ORGANISM: Homo sapiens  
31 <220> FEATURE:  
32 <221> NAME/KEY: CDS  
33 <222> LOCATION: (54)..(512)  
34 <223> OTHER INFORMATION:  
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38 Met  
39 1  
41 tgt tcc ctc ccc atg gca aga tac tac ata att aaa tat gca gac cag 104  
42 Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys Tyr Ala Asp Gln  
43 5 10 15  
45 aag gct cta tac aca aga gat ggc cag ctg ctg gtg gga gat cct gtt 152  
46 Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val Gly Asp Pro Val  
47 20 25 30  
49 gca gac aac tgc tgt gca gag aag atc tgc aca ctt cct aac aga ggc 200  
50 Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Thr Leu Pro Asn Arg Gly  
51 35 40 45  
53 ttg gac cgc acc aag gtc ccc att ttc ctg ggg atc cag gga ggg agc 248  
54 Leu Asp Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln Gly Gly Ser  
55 50 55 60 65  
57 cgc tgc ctg gca tgt gtg gag aca gaa gag ggg cct tcc cta cag ctg 296  
58 Arg Cys Leu Ala Cys Val Glu Thr Glu Gly Pro Ser Leu Gln Leu  
59 70 75 80  
61 gag gat gtg aac att gag gaa ctg tac aaa ggt ggt gaa gag gcc aca 344  
62 Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu Glu Ala Thr  
63 85 90 95  
65 cgc ttc acc ttc ttc cag agc agc tca ggc tcc gcc ttc agg ctt gag 392  
66 Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala Phe Arg Leu Glu  
67 100 105 110  
69 gct gct gcc tgg cct ggc tgg ttc ctg tgt ggc ccg gca gag ccc cag 440

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73 cag cca gta cag ctc acc aag gag agt gag ccc tca gcc cgt acc aag      488
74 Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser Ala Arg Thr Lys
75 130      135      140      145
77 ttt tac ttt gaa cag agc tgg tag ggagacagga aactgcgttt tagccttggt      542
78 Phe Tyr Phe Glu Gln Ser Trp
79      150
81 cccccaaacc aagctcatcc tgctcagggt ctatggtagg cagaataatg tccccgaaa      602
83 tatgtccaca tcctaattccc aagatctgtg catatgttac catacatgtc caaagagggt      662
85 ttgcaaagt gattatgtta aggatcttga aatgaggaga caatcctggg ttatccttgt      722
87 gggctcagtt taatcacaag aaggaggcag gaaggagagag tcagagagag aatggaagat      782
89 accatgcttc taattttgaa gatggagtga ggggccttga gccaacatat gcagggtgttt      842
91 ttagaaggag gaaaagccaa ggaacggat tctctcttat agtctccgga aggaacacag      902
93 ctcttgacac atggatttca gctcagtgac acccatttca gacttctgac ctccacaact      962
95 ataaaataat aaacttgtgt tattgtaaac ctctgg      998
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99 <211> LENGTH: 152
100 <212> TYPE: PRT
101 <213> ORGANISM: Homo sapiens
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109 Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val Gly Asp Pro
110      20      25      30
113 Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Thr Leu Pro Asn Arg
114      35      40      45
117 Gly Leu Asp Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln Gly Gly
118      50      55      60
121 Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro Ser Leu Gln
122 65      70      75      80
125 Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu Glu Ala
126      85      90      95
129 Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala Phe Arg Leu
130      100      105      110
133 Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu Pro
134      115      120      125
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142 145      150
145 <210> SEQ ID NO: 3
146 <211> LENGTH: 998
147 <212> TYPE: DNA
148 <213> ORGANISM: Homo sapiens
150 <220> FEATURE:
151 <221> NAME/KEY: CDS
152 <222> LOCATION: (3)..(512)
153 <223> OTHER INFORMATION:

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155 <400> SEQUENCE: 3
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157   Phe Gln Glu Leu Arg Ile Cys Ser Glu Asp Gln Thr Pro Leu Ile
158   1          5          10          15
160 gca gga atg tgt tcc ctc ccc atg gca aga tac tac ata att aaa tat      95
161 Ala Gly Met Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys Tyr
162          20          25          30
164 gca gac cag aag gct cta tac aca aga gat ggc cag ctg ctg gtg gga      143
165 Ala Asp Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val Gly
166          35          40          45
168 gat cct gtt gca gac aac tgc tgt gca gag aag atc tgc aca ctt cct      191
169 Asp Pro Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Thr Leu Pro
170          50          55          60
172 aac aga ggc ttg gac cgc acc aag gtc ccc att ttc ctg ggg atc cag      239
173 Asn Arg Gly Leu Asp Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln
174          65          70          75
176 gga ggg agc cgc tgc ctg gca tgt gtg gag aca gaa gag ggg cct tcc      287
177 Gly Gly Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro Ser
178 80          85          90          95
180 cta cag ctg gag gat gtg aac att gag gaa ctg tac aaa ggt ggt gaa      335
181 Leu Gln Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu
182          100          105          110
184 gag gcc aca cgc ttc acc ttc ttc cag agc agc tca ggc tcc gcc ttc      383
185 Glu Ala Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala Phe
186          115          120          125
188 agg ctt gag gct gct gcc tgg cct ggc tgg ttc ctg tgt ggc ccg gca      431
189 Arg Leu Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala
190          130          135          140
192 gag ccc cag cag cca gta cag ctc acc aag gag agt gag ccc tca gcc      479
193 Glu Pro Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser Ala
194          145          150          155
196 cgt acc aag ttt tac ttt gaa cag agc tgg tag ggagacagga aactgcgttt      532
197 Arg Thr Lys Phe Tyr Phe Glu Gln Ser Trp
198 160          165
200 tagccttggtg cccccaacc aagctcatcc tgctcagggt ctatggtagg cagaataatg      592
202 tcccccgaaa tatgtccaca tcctaataccc aagatctgtg catatgttac catacatgtc      652
204 caaagagggtt ttgcaaagt gattatgtta aggatcttga aatgaggaga caatcctggg      712
206 ttatccttgt gggctcagtt taatcacaag aaggaggcag gaaggagagag tcagagagag      772
208 aatggaagat accatgcttc taattttgaa gatggagtga ggggccttga gccaacatat      832
210 gcagggtgttt ttagaaggag gaaaagccaa ggggaacggat tctcctctat agtctccgga      892
212 aggaacacag ctcttgacac atggatttca gctcagtgac acccatttca gacttctgac      952
214 ctccacaact ataaaataat aaacttgtgt tattgtaaac ctctgg      998
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218 <211> LENGTH: 169
219 <212> TYPE: PRT
220 <213> ORGANISM: Homo sapiens
222 <400> SEQUENCE: 4
223 Phe Gln Glu Leu Arg Ile Cys Ser Glu Asp Gln Thr Pro Leu Ile Ala
224 1          5          10          15

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227 Gly Met Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys Tyr Ala
228          20          25          30
231 Asp Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val Gly Asp
232          35          40          45
235 Pro Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Thr Leu Pro Asn
236          50          55          60
239 Arg Gly Leu Asp Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln Gly
240 65          70          75          80
243 Gly Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro Ser Leu
244          85          90          95
247 Gln Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu Glu
248          100         105         110
251 Ala Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala Phe Arg
252          115         120         125
255 Leu Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu
256          130         135         140
259 Pro Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser Ala Arg
260 145         150         155         160
263 Thr Lys Phe Tyr Phe Glu Gln Ser Trp
264          165
267 <210> SEQ ID NO: 5
268 <211> LENGTH: 155
269 <212> TYPE: PRT
270 <213> ORGANISM: Homo sapiens
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277 Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His
278          20          25          30
281 Ala Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg
282          35          40          45
285 Trp Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly
286          50          55          60
289 Ser Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu
290 65          70          75          80
293 Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys
294          85          90          95
297 Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu
298          100         105         110
301 Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu Ala Asp
302          115         120         125
305 Gln Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp Asn Ala
306          130         135         140
309 Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp
310 145         150         155
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314 <211> LENGTH: 178
315 <212> TYPE: PRT
316 <213> ORGANISM: Rattus rattus

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318 <400> SEQUENCE: 6
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327 Pro Cys Lys Met Gln Ala Phe Arg Ile Trp Asp Thr Asn Gln Lys Thr
328 35 40 45
331 Phe Tyr Leu Arg Asn Asn Gln Leu Ile Ala Gly Tyr Leu Gln Gly Pro
332 50 55 60
335 Asn Thr Lys Leu Glu Glu Lys Ile Asp Met Val Pro Ile Asp Phe Arg
336 65 70 75 80
339 Asn Val Phe Leu Gly Ile His Gly Gly Lys Leu Cys Leu Ser Cys Val
340 85 90 95
343 Lys Ser Gly Asp Asp Thr Lys Leu Gln Leu Glu Glu Val Asn Ile Thr
344 100 105 110
347 Asp Leu Asn Lys Asn Lys Glu Glu Asp Lys Arg Phe Thr Phe Ile Arg
348 115 120 125
351 Ser Glu Thr Gly Pro Thr Thr Ser Phe Glu Ser Leu Ala Cys Pro Gly
352 130 135 140
355 Trp Phe Leu Cys Thr Thr Leu Glu Ala Asp His Pro Val Ser Leu Thr
356 145 150 155 160
359 Asn Thr Pro Lys Glu Pro Cys Thr Val Thr Lys Phe Tyr Phe Gln Glu
360 165 170 175
363 Asp Gln
367 <210> SEQ ID NO: 7
368 <211> LENGTH: 177
369 <212> TYPE: PRT
370 <213> ORGANISM: Sus scrofa
372 <400> SEQUENCE: 7
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375 1 5 10 15
378 Phe Leu Phe His Ser Glu Thr Ala Cys His Pro Leu Gly Lys Arg Pro
379 20 25 30
382 Cys Arg Met Gln Ala Phe Arg Ile Trp Asp Val Asn Gln Lys Thr Phe
383 35 40 45
386 Tyr Leu Arg Asn Asn Gln Leu Val Ala Gly Tyr Leu Gln Gly Pro Asn
387 50 55 60
390 Thr Lys Leu Glu Glu Lys Ile Asp Val Val Pro Val Glu Pro His Phe
391 65 70 75 80
394 Val Phe Leu Gly Ile His Gly Gly Lys Leu Cys Leu Ser Cys Val Lys
395 85 90 95
398 Ser Gly Asp Glu Met Lys Leu Gln Leu Asp Ala Val Asn Ile Thr Asp
399 100 105 110
402 Leu Arg Lys Asn Ser Glu Gln Asp Lys Arg Phe Thr Phe Ile Arg Ser
403 115 120 125
406 Asp Ser Gly Pro Thr Thr Ser Phe Glu Ser Ala Ala Cys Pro Gly Trp
407 130 135 140
410 Phe Leu Cys Thr Ala Leu Glu Ala Asp Gln Pro Val Gly Leu Thr Asn
411 145 150 155 160

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VERIFICATION SUMMARY

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